NCBI Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix [BLOSUM62 ▾] gap open: [11] gap extension: [1]
x_dropoff: [50] expect: [10.000] wordsize: [3] Filter ☑ View option [Standard ▾]
Masking character option [X for protein, n for nucleotide ▾] Masking color option [Black ▾]
☐ Show CDS translation [Align]

Sequence 1: gi|20072897|gb|AAH26175.1|ATF2 protein [Homo sapiens]
Length = 209 (1 .. 209)

Sequence 2: gi|22538422|ref|NP_001871.2|activating transcription factor 2 [Homo sapiens]
Length = 505 (1 .. 505)
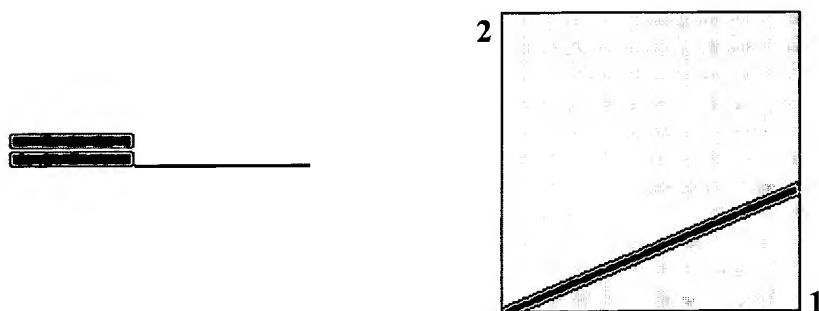
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  422 bits (1084),  Expect = 9e-117
 Identities = 209/209 (100%), Positives = 209/209 (100%), Gaps = 0/209 (0%)

Query   1    MKFKLHVNSARQYKDLWNMSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFGPARN    60
             MKFKLHVNSARQYKDLWNMSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFGPARN
Sbjct   1    MKFKLHVNSARQYKDLWNMSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFGPARN    60

Query   61   DSVIVADQTPTPTRFLKNCEEVGLFNELASPFENEFKKASEDDIKKMPLDLSPLATPIIR   120
             DSVIVADQTPTPTRFLKNCEEVGLFNELASPFENEFKKASEDDIKKMPLDLSPLATPIIR
Sbjct   61   DSVIVADQTPTPTRFLKNCEEVGLFNELASPFENEFKKASEDDIKKMPLDLSPLATPIIR   120

Query   121  SKIEEPSVVETTHQDSPLPHPESTTSDEKEVPLAQTAQPTSAIVRPASLQVPNVLLTSSD   180
             SKIEEPSVVETTHQDSPLPHPESTTSDEKEVPLAQTAQPTSAIVRPASLQVPNVLLTSSD
Sbjct   121  SKIEEPSVVETTHQDSPLPHPESTTSDEKEVPLAQTAQPTSAIVRPASLQVPNVLLTSSD   180

Query   181  SSVIIQQAVPSPTSSTVITQAPSSNRPIV    209
             SSVIIQQAVPSPTSSTVITQAPSSNRPIV
Sbjct   181  SSVIIQQAVPSPTSSTVITQAPSSNRPIV    209
```

```
CPU time:        0.03 user secs.         0.01 sys. secs         0.04 total secs.

Lambda       K       H
    0.312     0.127     0.366

Gapped
Lambda       K       H
    0.267     0.0410     0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 1185
Number of extensions: 607
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 209
Length of database: 1,302,931,322
Length adjustment: 127
Effective length of query: 82
Effective length of database: 1,302,931,195
Effective search space: 106840357990
Effective search space used: 106840357990
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.9 bits)
S2: 75 (33.5 bits)
```